What is claimed:

1. A method for modifying a polypeptide-encoding nucleotide sequence, the method comprising

providing a first polypeptide-encoding nucleotide sequence, wherein said polypeptide-encoding nucleotide sequence includes a plurality of codons encoding a polypeptide sequence;

identifying a first secondary structure for said first polypeptide-encoding nucleotide sequence;

altering at least one nucleotide in said first polypeptide-encoding nucleotide sequence, thereby producing a second nucleotide sequence;

identifying a second secondary structure for said second nucleotide sequence; and

comparing said first secondary structure and said second secondary structure, thereby modifying a polypeptide-encoding nucleotide sequence.

2. The method of claim 1, wherein said second secondary structure is different than said first secondary structure.

3. The method of claim 2, wherein the second secondary structure is more stable than the first secondary structure.

4. The method of claim 2, wherein the second secondary structure is less stable than the first secondary structure.

5. The method of claim 2, wherein base-pairing in at least one region of the second nucleotide sequence is altered relative to the corresponding region in the first polypeptide-encoding sequence.

6. The method of claim 5, wherein said region is 5-105 nucleotides.

7. The method of claim 5, wherein said region is 15-85 nucleotides.

8. The method of claim 5, wherein said region is 25-75 nucleotides.

9. The method of claim 1, wherein said at least one altered nucleotide is in a codon of said first polypeptide-encoding polynucleotide.

10. The method of claim 9, wherein said at least one altered nucleotide alters the number of cytosine and guanine nucleotides in said at least one altered codon.

11. The method of claim 10, wherein said at least one altered nucleotide results in an increased number of cytosine and guanine nucleotides in said codon.

12. The method of claim 10, wherein said at least one altered nucleotide results in an decreased number of cytosine and guanine nucleotides in said codon.

13. The method of claim 10, wherein said alteration changes at least two codons in said first polypeptide-encoding sequence.

14. The method of claim 10, wherein said alteration changes at least five codons in said first polypeptide-encoding sequence.

15. The method of claim 10, wherein said alteration changes at least ten codons in said first polypeptide-encoding sequence.

16. The method of claim 10, wherein said alteration changes at least 50 codons in said first polypeptide-encoding sequence.

17. The method of claim 1, wherein said first polypeptide-encoding nucleotide sequence is DNA.

18. The method of claim 1, wherein said first polypeptide-encoding nucleotide sequence is RNA.

19. The method of claim 1, wherein said second nucleotide sequence encodes a polypeptide having the same polypeptide sequence as the polypeptide sequence encoded by the first polypeptide-encoding nucleotide sequence.

20. A method for modifying a polypeptide-encoding nucleotide sequence, the method comprising

providing a first polypeptide-encoding nucleotide sequence from a first organism, wherein said polypeptide-encoding nucleotide sequence includes a plurality of codons encoding a polypeptide sequence;

identifying the frequency at which a first codon of said first polypeptide-encoding nucleotide sequence occurs in polypeptide-encoded genes of said first organism; and

replacing at least one nucleotide in said first codon, thereby producing a second nucleotide sequence including a first replacement codon, wherein said first replacement codon occurs at a different frequency in polypeptide-encoded genes of said first organism than said first codon,

thereby modifying a polypeptide-encoding nucleotide sequence.

21. The method of claim 20, wherein said first replacement codon occurs at a lower frequency in polypeptide-encoding genes of said first organism than said first codon.

22. The method of claim 20, wherein said first replacement codon occurs at a higher frequency in polypeptide-encoding genes of said first organism than said first codon.

23. The method of claim 20, wherein said first replacement codon encodes an amino acid identical to the amino acid encoded by said first codon.

24. The method of claim 20, wherein said method further comprises

identifying the frequency at which a second codon of said first polypeptide-encoding nucleotide sequence occurs in polypeptide-encoded genes of said first organism; and

replacing at least one nucleotide in said second codon, thereby producing a second nucleotide sequence including a second replacement codon, wherein said second replacement codon occurs at a different frequency in polypeptide-encoded genes of said first organism than said first codon.

25. The method of claim 24, wherein said second codon is adjacent to said first codon in said first polypeptide-encoding polynucleotide sequence.

26. The method of claim 20, wherein said second nucleotide sequence encodes an RNA molecule translated at a different rate than an RNA molecule encoded by said first polypeptide-encoding nucleotide sequence.

27. The method of claim 26, wherein said second nucleotide sequence encodes an RNA molecule that is translated more rapidly than said first polypeptide-encoding nucleotide sequence.

28. The method of claim 26, wherein said second nucleotide sequence encodes an RNA molecule that is translated more slowly than said first polypeptide-encoding nucleotide sequence.

29. The method of claim 20, further comprising

identifying the frequency at which said first codon occurs in polypeptide-encoded genes of a second organism; and

replacing at least one nucleotide in said first codon to produce a first replacement codon.

30. The method of claim 29, wherein said second codon occurs at a similar frequency in said second organism as the first codon occurs in the polypeptide-encoded genes of said first organism.

31. A method for modifying a polypeptide-encoding nucleotide sequence, the method comprising

providing a first polypeptide-encoding nucleotide sequence, wherein said polypeptide-encoding nucleotide sequence includes a plurality of codons encoding a polypeptide sequence;

identifying the guanine- cytosine content of a first codon in said polypeptide-encoding sequence;

replacing at least one nucleotide in said first codon, thereby producing a second nucleotide sequence including a first replacement codon, wherein said first replacement codon has a guanine-cytosine content different than said first codon, and wherein said first codon and said first replacement codon encode the same amino acids.

32. The method of claim 31, wherein said second polynucleotide sequence encodes an RNA molecule translated at a rate different than an RNA molecule encoded by said first polynucleotide sequence.

33. The method of claim 31, further comprising

identifying the guanine-cytosine content of a second codon in said polypeptide-encoding nucleotide sequence, and

replacing at least one nucleotide in said second codon, thereby producing a second nucleotide sequence including a second replacement codon, wherein said second replacement codon has a guanine-cytosine content different than said second codon, and wherein said second replacement codon and said second codon encode the same amino acids.

34. The method of claim 33, wherein said second codon is adjacent to said first codon.

35. A method for constructing a nucleic acid for increasing expression of a polypeptide-encoding nucleotide sequence, the method comprising

identifying codon frequencies of a polypeptide-encoding nucleotide sequence and codon frequencies in polypeptide-encoded genes of a first cell;

comparing said codon frequencies, thereby identifying at least one rare codon that is abundant in said transgene and occurs in low frequency in polypeptide-encoded genes of said cell; and

constructing an episomal vector comprising a tRNA gene with an anticodon for said rare codon, thereby constructing a nucleic acid for increasing expression of a polypeptide-encoding nucleotide sequence.

36 The method of claim 35, further comprising identifying codon frequencies of a second rare codon and constructing an episomal vector comprising a tRNA gene with an anticodon for said second rare codon.

37. The method of claim 33, wherein said host cell is a prokaryotic cell.

38. The method of claim 33, wherein said prokaryotic cell is an *E. coli* cell.

39. A cell that includes the episomal vector of claim 35.